

In the Abstract

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Abstract

Versions of the invention are directed to methods (including software), apparatus, and compositions of matter for new types of association-based linkage studies using bi-allelic markers. The bi-allelic markers used in the new linkage studies are chosen based on using the principle that the power of association-based linkage tests to detect linkage is greatly increased as the population allele frequencies of a bi-allelic trait-causing allele and a positively associated bi-allelic marker allele become similar in magnitude. The markers for these new linkage study techniques are selected based on each marker's chromosomal location and allele frequencies relative to the possible or known chromosomal location and allele frequencies of one or more possible trait-causing polymorphisms. By using the "two dimensions" of marker/polymorphism chromosomal location and allele frequency together, the power and systematic nature of association-based linkage studies is increased. These techniques are also effective for markers or trait-causing polymorphisms that are not bi-allelic.